

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 16.04 Seconds
(without alignments)
1491.198 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Sequence: 1 MATCIDTRCGRNTQDDSRF.....IPCLTMDQTSYLEWSPDYVI 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	2	S67482
2	1611	98.2	314	2	S71181
3	1215	74.0	391	2	S63192
4	1105	67.3	303	2	S68469
5	877	53.4	347	2	T09140
6	869	53.0	294	2	A57478
7	849.5	51.8	312	2	S71207
8	699	42.6	315	2	C81554
9	649.5	39.6	272	2	C81184
10	648.5	39.5	273	1	XFECSA
11	648.5	39.5	273	2	S29568
12	648.5	39.5	273	2	F86036
13	647.5	39.5	273	2	G83049
14	643	39.2	308	2	T08867
15	624.5	38.1	267	2	G64080
16	587.5	35.8	299	2	T04669
17	573.5	34.9	274	2	A84936
18	549.5	33.5	261	1	JC1293
19	472.5	28.8	270	2	T50058
20	442	26.9	225	1	E53402
21	424	25.8	217	1	B53402
22	422.5	25.7	227	2	T44913
23	420.5	25.6	249	1	S75606
24	409	24.9	251	2	T44279
25	405	24.7	229	2	H70660
26	395	24.1	229	2	F83663
27	392	23.9	258	2	A83169
28	389.5	23.7	199	2	E86856
29	388.5	23.7	212	2	C81347

30	369.5	22.5	269	1	D43706	serine O-acetyltra
31	365	22.2	171	1	B64671	serine O-acetyltra
32	359	21.9	171	2	B71845	o-serine acetyltra
33	338.5	20.6	220	2	G72349	serine acetyltrans
34	312	19.0	171	2	D84302	serine acetyltrans
35	287	17.5	319	2	S55322	srpH protein - Syn
36	265	16.1	231	2	H83381	probable acetyl tr
37	217	13.2	162	2	A64972	probable acetyl tr
38	217	13.2	162	2	B85832	probable transfera
39	207	12.6	184	2	C82264	serine acetyltrans
40	179	10.9	236	2	A86660	acetyltransferease
41	177.5	10.8	143	2	G82264	serine acetyltrans
42	175	10.7	236	2	H72245	2,3,4,5-tetrandro
43	175	10.7	240	2	E83983	tetrahydrodipicol
44	171	10.4	201	2	H85806	hypothetical prote
45	164.5	10.0	190	2	S07000	nodulation protein

ALIGNMENTS

RESULT 1

S67482

serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana

N/Alternate names: serine acetyltransferase

C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000

C/Accession: S67482; S52150

R/Rutifel, M.L.; Lebduh, M.; Droux, M.; Douce, R.

Eur. J. Biochem. 227, 500-509, 1995

A/Title: Subcellular distribution of serine acetyltransferase from Pisum sativum and

A/Reference number: S67482; MUID:95154333

A/Accession: S67482

A/Molecule type: DNA

A/Residues: 1-314 <RUF>

A/Cross-references: EMBL:Z34888; MID:9608676; PIDN:CAA84371.1; PID:9608677

A/Note: the authors translated the codon ACC for residue 158 as Ile and ACA for resid

C/Suprafamily: serine acetyltransferase; serine acetyltransferase homology

C/Keywords: acyltransferase; coenzyme A; cysteine biosynthesis

P:123-283/Domain: serine acetyltransferase homology <SAT>

Query Match	Best Local Similarity	100.0%;	Score 1641;	DB 2;	Length 314;
Matches 314;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MATCIDTRCGRNTQDDSRFCICINFRPGSVNRKIHHTQIEDDDVWIKMLEAKSDV	60		
DB	1	MATCIDTRCGRNTQDDSRFCICINFRPGSVNRKIHHTQIEDDDVWIKMLEAKSDV	60		
QY	61	KOEPLISVYVYASTSHRSLSALAHIIIVKLSNINLPNSTLFEFTSVLEESPEITEST	120		
DB	61	KOEPLISVYVYASTSHRSLSALAHIIIVKLSNINLPNSTLFEFTSVLEESPEITEST	120		
QY	121	KODLAVNERDPACISVYHCEFGKGFACQAHRIAHHTLMKONRKIVALLIONRVSSFA	180		
DB	121	KODLAVNERDPACISVYHCEFGKGFACQAHRIAHHTLMKONRKIVALLIONRVSSFA	180		
QY	181	VDIHGAKIGKIGILDHATGTVYIGETAVVGNVSTILHRYTIGTGKSGDRHPRKIGGVL	240		
DB	181	VDIHGAKIGKIGILDHATGTVYIGETAVVGNVSTILHRYTIGTGKSGDRHPRKIGGVL	240		
QY	241	IGAGSCIIIGNTIGGKAGIGSGSVVVKDVPARTAVGNPARIIGKENPRKHDPICITM	300		
DB	241	IGAGSCIIIGNTIGGKAGIGSGSVVVKDVPARTAVGNPARIIGKENPRKHDPICITM	300		
QY	301	DOTSYLTWSPDYVI 314			
DB	301	DOTSYLTWSPDYVI 314			
RESULT	2	S71181			

QY	192	GIL-LDHATGVIGETAVVGDNYSILHGVTLGGTQKSGDRHPKTIQDGVILGASGCIIGN	250
		// : : : : : : : :	
Db	182	GIFALDHATVIGETAVVGNVNSILHANTVLGGTGQCCDRHPKTIQDGVYL--GYCLIGN	239
QY	251	ITIEGAKIGSGSVVVKDVPARTTAVGNPARLIGCKREPKRDKTIPCLTMDOTSITEMS	310
		: : : : : : : : :	
Db	240	ITIEGAKIGSGSVLKEYEPGTTVVGNPRLIGCKRDKPTKIDKTIPLGTLMDOTSITEMS	299
QY	311	DYVI 314	
Db	300	DYVI 303	

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RESULT      5
T09140
N:serine O-acetyltransferase (EC 2.3.1.30) - spinach
C:Alternate names: serine acetyltransferase
C:Species: Spinacia oleracea (spinach)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
C:Accession: T09140
R:Saito, K.; Takagi, Y.
submitted to the EMBL Data Library, October 1996
A:Description: A cDNA encoding serine acetyltransferase from spinach.
A:Reference number: Z16582
A:Accession: T09140
A:Status: preliminary, translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-347 <SAT>
A:Cross-references: EMBL:D88529
A:Experimental source: leaf
C:Function:
A:Description: catalyzes conversion of L-serine to O-acetyl serine (by acetyl CoA)
A:Pathway: cysteine biosynthesis
C:Superfamily: serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F:136-316/Domain: serine acetyltransferase homology <SAT>

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	Query Match	53.4%;	Score 877;	DB 2:	Length 347;	
	Best Local Similarity	56.6%;	Pred. No.2.9e-65;			
	Matches 163; Conservative	53;	Mismatches 70;	Indels 2;	Gaps 1.	
Qy	PG-FSVNRKIHHTQIEDDDVVMKMLEAKADYOEPLTSNYYYASTSHRSLESALAH	86				
Dd	PGGDLSVAPSVCHLIRANNPAMIMDQIKGARRDABSEPRALASTLYSTILSHSLEMSLSF	119				
Qy	ILSVKLNLNLPNSLT.FELFELSVESEPRIESTKODLIIVAEKRPACISYVHCFEGFG	146				
Dd	HIGNLKCSSTLLSTLLDYDFLNILSSDSLLDAVVADLAARVRDPACYSFSHCLLNTYNG	179				
Qy	FLTCAQHRIAHTLMKONRKIVALLLIONRVSESFAVDIHFAGAKIGKGLIDHATGVYTGET	206				
Dd	FLACOSHRVAHKMLMODRRRLPALALHSRISDYFAEADIHPAARIGKGLIDHATGVYTGET	239				
Qy	AVYGDNVSILLHGVTLAGGTGKSGDRPKIGDGYVLGAGSCIIENITLGAGATIGSSVYV	266				
Dd	AATIGDNCSILLHVTLGGTGKAGGRHPKYGDEVLLIGAGATILGNARIIGAKAIGAGSVYL	299				
Qy	KIVPARATTWGNPARRLIGGENDKRDKJPCJLMOOTSLTEKSSDVI	314				
Dd	IIVPTTTAVGNPARRLIGGEKEPSQSDVPAGESMDHTSIENSESDIII	347				

RESULT 6
A57478
serine O-acetyltransferase (EC 2.3.1.30) - watermelon
C:Species: Citrullus lanatus (watermelon)
C:Date: 08-Dec-1995 #sequence (revision 08-Dec-1995 #text_change 20-Jun-2000
C:Accession: A57478
R:Salto, K.; Yokoyama, H.; Noji, M.; Murakoshi, I.
J. Biol. Chem. 270, 16321-16326, 1995
A:Title: Molecular cloning and characterization of a plant serine acetyltransferase play
A:Reference number: A57478; MUID:95332343

A:Accession: A57478
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-294 <SAI>
A:CROSS-references: GB:049535; NID:q1060871; PID:BAA08479.1; PID:q1841312
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A
F:103-253/Domain: serine acetyltransferase homology <SAT>

[illegible]

RESULT 7
S71207
serine O-acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
C:Accession: S71207
R:Howarth, J.R.; Roberts, M.A.; Wray, J.L.
submitted to the EMBL Data Library, June 1995
A:Description: Cysteine biosynthesis in higher plants: a novel cDNA clone for serine
A:Reference number: S71207
A:Accession: S71207
A:Molecule type: mRNA
A:Residues: 1-312 <HOW>
A:Cross-References: EMBL:U30298; NID:g905390; PIDN:AMC49655.1; PID:g905391
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F:120-280/Domain: serine acetyltransferase homology <SAT>

	Query Match	51.8%	Score 849, 5;	DB 2;	Length 312;
	Best Local Similarity	59.7%;	Pred. No. 4, 9e6;		
	Matches 160; Conservative	45;	Mismatches 62;	Indels 1;	Gaps
<hr/>					
Qy	48	VWIKMLEAKSDVKOEPIILSNYYASTSHRSLSALAHILSVKLSMLNPSTLPEFLT	107		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Dd	45	LWTQIAKEARRRAEAPALASTYSTIISHSLERSFSHGNLKCSSTLTSLTYDLFL	104		
<hr/>					
Qy	.108	SVLESPEITESTKODLIAVKEPDACISYVHCFFGFGLACANHIAHTLMKONRIV	167		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Dd	105	NPFSSDPSIRMAVTADLRARARDPACISFESHCLINTKYGLAIDAHNVSKHLWQNSKPL	164		
<hr/>					
Qy	168	ALLIONRVSESPAVDIHPGAKIGKILLDHATGVVIGETFAVGDNVSILHGVTIGTGKO	227		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Dd	165	ALATSRIKDPAVDVHPAAKIGKILLDHAHTGVVVGETAVIGNANVISLHHVTIGGTGA	224		
<hr/>					
Qy	228	SDDRHKKIGDGVLICAGSCIIINLTIGEGAKIGSGSVVKKVPARTAVNGPARLIGKE	287		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Dd	225	CGRHKRTIDGGCLTAGATILLNVAITGCAKVGSASVLLDVPCRGTAIVNGPARLVGKE	284		

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: A65161

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <BLAT>

A:Cross-references: GB:AE000438; GB:U00096; NID:q2367251; PIDN:AC76631.1; PID:91790035;

A:Experimental source: strain K-12, substrain MG1655

C:Comment: This enzyme catalyzes the conversion of L-serine to O-acetyl serine (by acetyl

C:Genetics:

A:Gene: *cysE*

A:Map position: 81 min

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: aminoacyltransferase; coenzyme A; cysteine biosynthesis

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 1; Length 273;

Best Local Similarity 50.8%; Pred. No. 2e-46;

Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMLEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNMLPSNTL 102

DB 4 EELEIWNKIKAEARTLADCEPMILASFYHATLLKHENLGSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISVHCFLEFGFGLACQAHRIAHITLTKQ 162

DB 64 REVEEAAYADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALLIONRVSESPAVDHPGAKIGKGLLDHATGVIGETAVGVNDVSTLHGVTIG 222

DB 124 GRRLAALFLQNOVSVTFQVDIHPAKIGRIGIMLDHATGIVGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 282

DB 184 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 243

QY 283 IGGKPNRKHDKIPCLTMDQ 302

DB 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 11

S29368

serine O-acetyltransferase (EC 2.3.1.30) - *Salmonella typhimurium*

C:Species: *Salmonella typhimurium*

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S29368

R:Siivprasad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.

submitted to the EMBL Data Library, May 1991

A:Description: A novel biosynthetic pathway for mammalian cells by stable integration of

A:Reference number: S29367

A:Accession: S29368

A:Molecule type: DNA

A:Residues: 1-273 <SI>

A:Cross-references: EMBL:X59594; NID:q47659; PIDN:CAA42163.1; PID:947660

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: acyltransferase; coenzyme A

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 2; Length 273;

Best Local Similarity 51.2%; Pred. No. 2e-46;

Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMLEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNMLPSNTL 102

DB 4 EELEIWNKIKAEARTLADCEPMILASFYHATLLKHENLGSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISVHCFLEFGFGLACQAHRIAHITLTKQ 162

DB 64 REVEEAAYADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALLIONRVSESPAVDHPGAKIGKGLLDHATGVIGETAVGVNDVSTLHGVTIG 222

DB 124 GRRLAALFLQNOVSVTFQVDIHPAKIGRIGIMLDHATGIVGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 282

DB 184 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 243

QY 283 IGGKPNRKHDKIPCLTMDQ 302

DB 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 12

serine acetyltransferase [imported] - *Escherichia coli* (strain 0157:H7)

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: F66036

P:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F66036

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-273 <STO>

A:Cross-references: GB:AE005174; NID:q12518357; PIDN:AAG58754.1; GSPDB:GN00145; UMGF:

A:Experimental source: strain 0157:H7, substrain EDL933

C:Genetics:

A:Gene: *cysE*

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

Query Match 39.5%; Score 648.5; DB 2; Length 273;

Best Local Similarity 50.8%; Pred. No. 2e-46;

Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMLEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNMLPSNTL 102

DB 4 EELEIWNKIKAEARTLADCEPMILASFYHATLLKHENLGSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISVHCFLEFGFGLACQAHRIAHITLTKQ 162

DB 64 REVEEAAYADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALLIONRVSESPAVDHPGAKIGKGLLDHATGVIGETAVGVNDVSTLHGVTIG 222

DB 124 GRRLAALFLQNOVSVTFQVDIHPAKIGRIGIMLDHATGIVGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 282

DB 184 GTGKSGDRHPKIRIGVILGAGSCILGNTTIGEGAKIGSGSVVVKVDPARTAVGNPARI 243

QY 283 IGGKPNRKHDKIPCLTMDQ 302

DB 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 13

serine acetyltransferase VC2649 [imported] - *Vibrio cholerae* (strain N16961 serogroup

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82049

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.

Charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers

L.R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A>Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833

